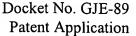


- 23. The method according to claim 22, wherein the enzyme is a polymerase enzyme.
- 24. The method according to claim 22, wherein the enzyme is a helicase enzyme or a primase enzyme.
- 25. The method according to claim 22, wherein the enzyme is immobilised on a solid support.
- 26. The method according to claim 25, comprising a plurality of enzymes immobilised on the solid support.
- 27. The method according to claim 22, wherein the enzyme comprises a first bound detectable label, the characteristics of which alter as the enzyme undergoes a conformational change.
- 28. The method according to claim 27, wherein the enzyme comprises a second bound detectable label capable of interacting with the first label, wherein the degree of interaction is dependent on a conformational change in the enzyme.
- 29. The method according to claim 27, wherein a second detectable label is bound to a nucleotide brought into contact with the enzyme.
- 30. The method according to claim 28, wherein the first label is an energy acceptor and the second label is an energy donor, or wherein the first label is an energy donor and the second label is an energy acceptor, and wherein step (ii) is carried out by measuring energy transfer between the two labels.





- 31. The method according to claim 29, wherein the first label is an energy acceptor and the second label is an energy donor, or wherein the first label is an energy donor and the second label is an energy acceptor, and wherein step (ii) is carried out by measuring energy transfer between the two labels.
- 32. The method according to claim 22, wherein step (ii) is carried out using confocal microscopy.
- 33. The method according to claim 32, wherein step (ii) is carried out by fluorescence imaging.
- 34. The method according to claim 27, wherein step (ii) is carried out by measuring a polarisation effect consequent on the altered characteristics of the first label.
- 35. The method according to claim 34, wherein step (ii) is carried out by fluorescence polarisation anisotrophy.
- 36. A method for determining the sequence of a polynucleotide, comprising detecting via fluorescence resonance energy transfer a conformational change in an enzyme that interacts with and processes along a target polynucleotide, thereby permitting determining the sequence of the polynucleotide.
 - 37. The method according to claim 36, wherein the enzyme is a polymerase enzyme.
- 38. The method according to claim 36, wherein the enzyme is immobilised on a solid support.
- 39. The method according to claim 37, wherein the enzyme is immobilised on a solid support.





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- 40. A method for determining the sequence of a polynucleotide, comprising detecting a detectably-labelled enzyme that is capable of interacting with and processing along a target polynucleotide, wherein the label alters its detectable characteristics as the enzyme processes along the polynucleotide, thereby permitting determining the sequence of the polynucleotide.
- 41. A solid support comprising at least one immobilised enzyme capable of interacting with and processing along a target polynucleotide, the enzyme being labelled with one or more detectable labels.
 - 42. The solid support according to claim 41, wherein the enzyme is a polymerase.
 - 43. The solid support according to claim 41, wherein the label is a fluorophore.
 - 44. The solid support according to claim 42, wherein the label is a fluorophore.
- 45. A system for determining a sequence of a polynucleotide, comprising a solid support according to claim 41, and an apparatus for detecting the label.

